A SYSTEMATIC WAY OF DEVELOPING A COVID-19 REINFECTION MODEL USING MATHEMATICAL MODEL APPROACH

ABSTRACT

In this paper, we present a mathematical model to analyze the compartmental transmission of Covid-19 and the phenomenon of reinfection among human populations. Our novel SVEQAITR model incorporates unique aspects of the disease, such as the presence of infectious but undetected cases and varying health conditions of hospitalized individuals. A significant innovation in our model is the assessment of detected cases in relation to the actual total infected cases, enabling an exploration of how this ratio affects the overall impact of COVID-19. This model is also capable of estimating hospital bed requirements. While it is sufficiently complex to capture critical dynamics, it remains straightforward enough for effective parameter identification using publicly available pandemic data. We demonstrate a strong correlation between our model's predictions and reported data. Additionally, we analyze how the model's outputs behave when applied to incomplete reported data—specifically, data truncated around the peak daily case counts. This comparison allows us to evaluate the modeling errors that arise when determining parameters during the early stages of the pandemic. Lastly, we explore various scenarios to illustrate how different detection rates could have influenced the overall scale of COVID-19 in China, providing valuable insights for policymakers. The COVID-19 pandemic became a significant global concern in the first half of 2020, prompting a surge of rapid research on its epidemiology, clinical presentation, diagnostic patterns, and prognosis.

Keywords: Covid-19, Reinfection, Mathematical model, Epidemiology

1 INTRODUCTION

Corona virus disease 2019 (COVID-19) is an infectious disease caused by Corona Virus 2 (SARS-CoV-2). Covid-19 is known to have symptoms such as fever, cough, fatigue, loss of senses of smell and taste, which can be extremely contagious and spread easily from person to person (Feng et al., 2020). It is transmitted through respiratory droplets, most commonly when coughing, sneezing, or in conversation. Most people infected with the Covid-19 virus experience mild to moderate respiratory illness, however older people with medical problems such as cardiovascular disease, diabetes, chronic respiratory disease, cancer, etc. are more likely to develop serious diseases (Kifle and Obsu, 2022). Scientists have proven that the COVID-19 pandemic is a global health crisis because it has caused disruptions in healthcare, economy, politics, society, and worldwide impact (Li et al. 2020). With the spread of the virus it is important to understand how it transmits and the possibility of getting re-infected. It presents challenges that require an understanding of different aspects of the disease. Although progress has been made in terms of vaccination efforts and understanding how infections occur and spread, reinfection cases continue to be a concern. These cases not only raise questions about how immunity lasts after an initial infection, but also have implications for vaccination effectiveness and future management strategies (Bubar et al. 2020). The study revealed that reinfection can occur in older people, while the rate of transmission will be reduced in teenagers. The first case of COVID-19 with reinfection is reported after two months of complete recovery from SARS-COV-2 infection (Hanif et al., 2020). Due to the emergence of the omicron variant, several cases of reinfection are documented and it is further documented that 35,670 out of 2,796, 982 individuals with confirmed laboratory SARS-COV-2 cases are found to have been reinfected (Atifa et

al., 2022).
Mathematical modeling in science and engineering has a vital role to play in understanding the complex behaviors of the problems arising in physical and biological modeling; see, for example, disease epidemiology (Li et al., 2021a; Okuonghae and Omame, 2020), in fluid-related studies (Chu et al., 2021; Li et al., 2021b). Observing from the above facts on the reinfection of COVID-19 cases, the world may face a new number of infected cases and deaths. Before we formulate a new mathematical model to study the impact of SARS-COV-2 on reinfection, we first highlight some mathematical models that addressed COVID-19 infection.
The aim of this paper is to develop a mathematical model for COVID-19 with reinfection that incorporates Vaccination, Quarantine and Treatment compartments. We consider multiple factors, including viral evolution, individual immunity response, antigenic variation, and a host of susceptibility. By integrating biological and epidemiological data, mathematical models can account for these complex interactions and provide insight into the potential impact of reinfection on overall disease transmission and control strategies.

2 MATERIALS AND METHODS

In this paper, we study the epidemiology of Covid-19 with its reinfection using the Susceptible, Vaccinated, Exposed, Quarantined, Asymptomatically infected, Symptomatically infectious, Treatment and Recovered model. The results of the research will aid in predicting the risk factors affecting reinfection of Covid-19 and the optimum strategies to implement in order to prevent and control the spread and re-occurrence of the virus.

2.1 Mathematical Modeling

This is a process of describing a real-world problem in mathematical terms, usually in a form of differential equations. Using these differential equations will help to understand the original problem and also to discover new features about the problem. This method of modeling the transmission of infectious diseases was discovered by Bernoulli in 1760.
The two common types of mathematical modeling in this area are the Deterministic Model and the Stochastic model.

2.2 Deterministic Model

This is a type of mathematical model that gives an exact value or accurately predicts certain characteristics of an outcome as a function of parameters by using differential equations (Andrich, 2005). This model describes the dynamic interrelations among the rates of change and population sizes for the transmission process of an infectious disease using a compartmental approach.

2.3 DESCRIPTION OF THE SVEQAITR MODEL OF COVID-19 WITH REINFECTION

In applying the SVEQAITR model, we have succeeded in dividing the population into eight classes namely; The Susceptible class (S);
The Vaccinated class (V);
The Exposed class (E);
The Quarantined class (Q);
The Asymptomatically Infectious Class (A);
The Chronically Infectious Class (I);
The class undergoing treatment (T); and
The Removed class (R).

Susceptible class S consists of individuals who have yet to come in contact with the virus but are still capable of contracting the disease.
Vaccinated class V consists of people who have been vaccinated.
The exposed class E consists of individuals who are in their latent period of infection. This implies that they are the ones that have been infected with the virus but are incapable of spreading the virus.
Q Quarantine class consists of people who are already infected and are then isolated for a specified duration of 14 days to prevent the spread of the disease and ensure the safety of people.
The Asymptomatically Infectious Class A contains individuals who are infected but do not show any

noticeable symptoms of the Covid-19 virus and are capable of infecting the susceptible class.
Chronically infectious class I consists of people who have tested positive for the Covid-19 virus, as the symptoms clearly show.
The Treatment class T compartment contains people who are infected and infectious undergoing treatment.
The removed class R are those individuals that are permanently immune to the disease (either as a result of the vaccine or recovery while in the acute stage of the disease).

2.4 Assumptions of the Model

This model works on the following assumptions:

1. That the rate of disease transmission from asymptomatic infected individuals are less than that of the symptomatic infected and treated individuals $A(t) < \gamma_1(1-\tau)A < \gamma_2(1-\psi)I$;

2. That the symptomatic infected and treated individuals experience additional disease-induced death rate $I(t) - \delta_i, T(t) - \delta_r$;

3. That the asymptomatic infected disease-induced death rate δ is negligible;

4. All individuals are decreased by natural death rate $N - \mu N$;

5. Since there is currently no evidence that individuals develop permanent immunity against Covid-19. Therefore, it is assumed that the recovered individuals become susceptible again at the rate of ϕ; $(R - \phi_r)$

6. Quarantined individuals who do not show symptoms while in quarantine are transferred back to susceptible class at rate $\sigma(1-\theta)$ i. e, $(Q - \sigma(1-\theta))$;

7. That the symptomatic infected individuals can either be treated or recovered; i. e, $(I - \gamma_2(1-\psi)I)$ or $(I - \gamma_2 \psi I)$

8. That the vaccinated individuals can become exposed to the disease at $\beta_2(1-\varepsilon)$, meaning that vaccination wane after a short period of time thereby provides only partial protection against Covid-19; i e, $(V - \beta_2(1-\varepsilon))$

9. That recovered individuals can become re-infected again when they come in close contact with asymptomatic, symptomatic and treatment class because of the inefficacy of drugs i.e, $(R - \phi_r)$.

10. That all parameters in the model are assumed to be positive or non-negative.

Table 1. Description of variables and parameters in the Model.

PARAS	DEFINITION
Λ	Recruitment rates of humans into the Susceptible compartment
λ_1	Force of infection from susceptible to exposed compartment
λ_2	Force of infection from vaccinated to exposed compartment
β_1	Effective contact rate from susceptible to exposed compartment
β_2	Effective contact rate from vaccinated to exposed compartment
α_1	Progression rate of exposed individuals into the quarantined class
α_2	Progression rate of exposed individuals into the asymptomatic infectious class
α_3	Progression rate of exposed individuals into the symptomatic class
η	Vaccinated rate
σ	Rate of developing clinical symptoms during quarantine
ϕ	Rate at which individuals lose immunity
θ	Fraction of quarantine population that is treated
ε	Infection reduction of vaccinated individuals
τ	Proportion of asymptomatic who recover naturally
ψ	Proportion of infectious who recover naturally
γ_1	Exit rate from the asymptomatic class
γ_2	Exit rate from the infected class
γ_3	Recovery rate of treated individuals
μ	Natural death rate of individuals in the population under study
δ	Disease induced death rate

Fig. 1 represents the SVEQAITR model with vital dynamics.

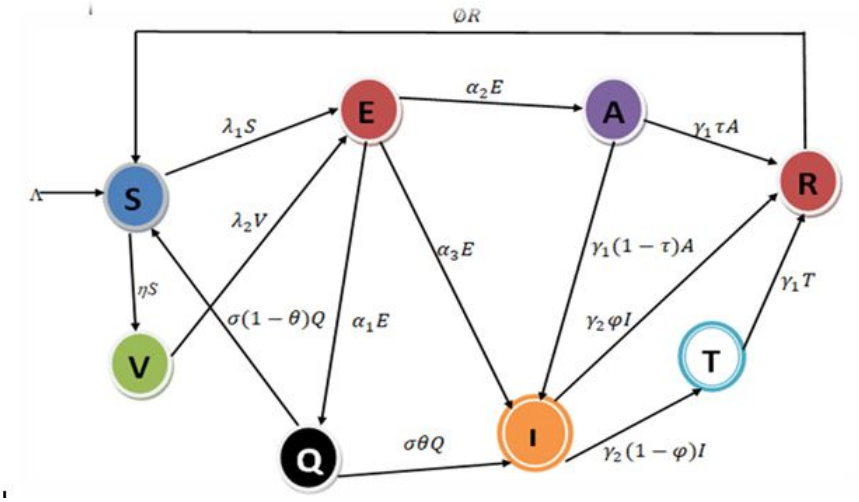

Figure 1. Nwagwu, modified Model flow chart

The Atifa et al. (2022) model is extended considering vaccination, quarantine, and treatment compartments, and it is assumed that quarantined individuals can be transferred back to the susceptible class, vaccinated individuals who lose immunity can progress to the exposed class, and treated individuals can recover or die as a result of the disease or a natural death, and using a deterministic compartmental modeling approach to describe the disease transmission dynamics. The total population size is subdivided into epidemiological subclasses: susceptible $S(t)$, vaccinated V(t), exposed $E(t)$, quarantine $Q(t)$, asymptomatic infectious $A(t)$, symptomatic infectious $I(t)$, treatment $T(t)$ and recovered $R(t)$.
The total population $N(t)$ is then given by:

$$N(t) = S(t) + V(t) + E(t) + Q(t) + A(t) + I(t) + T(t) + R(t) \tag{1}$$

Individuals are recruited into the population at a rate ΛS . V is the vaccination class since Covid-19 is biologically available, and then it is realistic to consider the vaccination class, η V is the transmission rate from susceptible to the vaccination class. $\lambda_1 S$ is the force of infection from susceptible to exposed class while $\lambda_2 V$ is the force of infection from vaccinated individuals to exposed class. $\beta_1(A+I+T)S$ and $\beta_2(1-\varepsilon)V$ are effective contact rates. ε represents the infection reduction of vaccinated individuals. $\alpha_1 E$ is the rate of exposure to quarantine,$\alpha_2 E$ is the rate of exposure to asymptomatic, and $\alpha_3 E$ is the rate of exposure to infectious class. The quarantined individuals increase as a result of the quarantining of individuals of the exposed class at the rate $\alpha_1 E$. Individuals who do not show symptoms while in quarantine are transferred back to the susceptible class at a rate of $\sigma(1-\theta)Q$, and individuals who showed Covid-19 symptoms while in quarantine are moved to the infectious class at a rate of $\sigma\theta Q$ for medical attention. Asymptomatic individuals are reduced by the natural death rate μ, but δ, which is death due to the disease in this class, is assumed to be negligible, because individuals in this class do not show Covid-19 symptoms but are fully infected. Those who develop Covid-19 symptoms are moved to the symptomatic class at a rate of $(1-\tau)$, while a fraction τ may recover naturally from asymptomatic infection and move to the recovered class R. Individuals exit the symptomatic infected class through the natural death rate μ and through death due to the disease δ. The fraction of $(1-\psi)$ is hospitalized for treatment while the fraction ψ recovers naturally. Finally, hospitalized individuals (T) are treated and recovered at a rate γ_3. Individuals also leave the treatment class through a natural death rate μ and through a death from the disease δ. We also consider that recovered individuals (R) die naturally μ and a fraction ϕ becomes susceptible (S) again because individuals lose permanent immunity to Covid-19 and are prone to reinfection. Considering the definitions, assumptions and interrelations between the variables and the parameters, the basic dynamics of Covid-19 re-infection is illustrated as a flow diagram in Figure 1.

From Figure 1, the following system of differential equations are obtained:

$$\frac{dS(t)}{dt} = \Lambda - (\lambda_1 + \eta + \mu)S + \sigma(1-\theta)Q + \phi R \tag{2a}$$

$$\frac{dV(t)}{dt} = \eta S - (\lambda_2 + \mu)V \tag{2b}$$

$$\frac{dE(t)}{dt} = \lambda_1 S + \lambda_2 V - (\alpha_1 + \alpha_2 + \alpha_3 + \mu)E \tag{2c}$$

$$\frac{dQ(t)}{dt} = \alpha_1 E - \sigma(1-\theta)Q - (\sigma\theta + \mu)Q \tag{2d}$$

$$\frac{dA(t)}{dt} = \alpha_2 E - (\gamma_1\tau + \mu)A - \gamma_1(1-\tau)A \tag{2e}$$

$$\frac{dI(t)}{dt} = \alpha_3 E + \sigma\theta Q - (\gamma_2\psi + \mu + \delta)I + \gamma_1(1-\tau)A - \gamma_2(1-\psi)I \tag{2f}$$

$$\frac{dT(t)}{dt} = \gamma_2(1-\psi)I - (\gamma_3 + \mu + \delta)T \tag{2g}$$

$$\frac{dR(t)}{dt} = \gamma_1\tau A + \gamma_2\psi I + \gamma_3 T - (\phi + \mu)R \tag{2h}$$

From equation (2a) the Susceptible compartment, people are recruited at a rate of Λ, there is an interaction with compartments Asymptomatic, Infectious and people on treatment, which is called the force of infection at the rate of λ_1, η is the transmission rate from Susceptible to Vaccinated people and μ is the natural death rate of Susceptible people. People in the quarantine compartment who do not show symptoms are transferred back to the susceptible compartment at rate of $\sigma(1-\theta)Q$ while people who recovers but over the time loses immunity gets reinfected again and goes back to the susceptible compartment at the rate of ϕ

From equation 2b (the vaccination compartment), susceptible people enter this compartment at a rate of η while λ_2 exits the compartment into the exposed compartment and the natural death μ.

From equation (2c) (the exposed compartment), susceptible and vaccinated people enter this compartment at the rate of λ_1 and λ_2 respectively, while some individuals exit the exposed compartment and enter into quarantine, Asymptomatic and Infectious compartments at the rate of α_1, α_2, and $alpha_3$ respectively and of course natural death μ

3 RESULT ANALYSIS

3.1 Boundedness of the solution

$$D = \{(S,V,E,Q,A,I,T,R) \in \Re^8_+, \leq \frac{\lambda}{\mu}\} \tag{3}$$

Theorem 1: There exists a domain in D in which the set of solutions $\{S,V,E,Q,A,I,T,R\}$ is contained and bounded (Daniel, 2020).
Proof: Given the solution set $\{S,V,E,Q,A,I,T,R\}$
$N = S+V+E+Q+A+I+T+R$
The total derivatives of human population is given by:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE}{dt} + \frac{dQ}{dt} + \frac{dA}{dlt} + \frac{dI}{dt} + \frac{dT}{dt} + \frac{dR}{dt} \tag{4}$$

Therefore, substituting (2a) - (2h) in (4) we obtain $\frac{dN}{dt}$ as;

$$\begin{aligned} &\frac{dN}{dt} = \Lambda - \mu(S+V+E+Q+A+I+T+R) - \delta(I+T), \\ &= \Lambda - \mu N - \delta(I+T) \leq \Lambda - \mu N \end{aligned} \tag{5}$$

This implies that $\frac{dN}{dt} \leq \Lambda - \mu N$
Rewriting (5) we have,

$$\frac{dN}{dt} + \mu N \leq \Lambda \tag{6}$$

Solving (6) using integrating factor method, we first of all find our integrating factor (I.F)
$I.F = \exp^{\int p(t)dt}$; let $p(t) = \mu$
$I.F = \exp^{\int \mu dt} = \exp^{\mu t}$
multiplying (6) by $\exp^{\mu t}$

$$\frac{dN}{dt}\exp^{\mu t} + \mu \exp^{\mu t} N \leq \Lambda \exp^{\mu t} \tag{7}$$

Rewriting (7) we will have;

$$\frac{d}{dt}(N\exp^{\mu t}) \leq \Lambda \exp^{\mu t} \tag{8}$$

Integrating (8) with respect to t we have;

$$N(t)\exp^{\mu t} \leq \int \Lambda \exp^{\mu t} dt \tag{9}$$

$$N(t) \leq \frac{1}{\exp^{\mu t}} \int \Lambda \exp^{\mu t} dt \tag{10}$$

$$
\begin{aligned}
N(t) &\leq \frac{\Lambda}{\exp^{\mu t}} \int \exp^{\mu t}\, dt \\
N(t) &\leq \frac{\Lambda}{\exp^{\mu t}} \left[\frac{1}{\mu} \exp^{\mu t} + K \right] \\
N(t) &\leq \frac{\Lambda}{\mu} + K \exp^{-\mu t}
\end{aligned}
\tag{11}
$$

As t $\to \infty, N(t) \leq \frac{\Lambda}{\mu}$.
Thus, all the solutions of the population are confined in the feasible region D. This shows that the solution of model (2) exists and is given by $D = \{(S,V,E,Q,A,I,T,R) \in \Re_{+8:N(t)\leq \frac{\Lambda}{\mu}}\}$.

3.2 Non-negativity of Solution

Theorem 2: Given the initial data $S(0) \geq 0, V(0) \geq 0, E(0) \geq 0, Q(0) \geq 0. A(0) \geq 0, I(0) \geq 0, T(0) \geq 0, R(0) \geq 0$ of the model (2) are non-negative for all time $t > 0$ (Abioye et al 2021).
Proof: Let $t_1 = sup\{S(0) > 0, V(0) > 0, E(0) > 0, Q(0) > 0. A(0) > 0, I(0) > 0, T(0) > 0, R(0) > 0\}$.
From (2a) of the model, we have ;

$$
\frac{dS}{dt} = \Lambda + \phi R + \sigma(1-\theta)Q - (\lambda_1 + \eta + \mu)S \tag{12}
$$

Rewriting (12) we now have,

$$
\frac{dS}{dt} + (\lambda_1 + \eta + \mu)S = \phi R + \sigma(1-\theta)Q \tag{13}
$$

Solving (13) using integrating factor we have,

$$
\frac{d}{dt}\left[S(t)(\exp^{\int_0^t (\lambda_1+\eta+\mu)dt}) \right] \qquad = \phi R + \sigma(1-\theta)Q \left[\exp^{\int_0^t (\lambda_1+\eta+\mu)dt} \right] \tag{14}
$$

Integrating from 0 to t_1 we have,

$$
\left[S(t_1) \left(\exp^{\int_0^t (\lambda_1+\eta+\mu)dt} \right) \right] - S(0) = \phi R + \sigma(1-\theta)Q \int_0^t i \left[\exp^{\int_0^x (\lambda_1+\eta+\mu)} \right] dx \tag{15}
$$

multiply (15) through by $exp^{-\int_0^{t_1} (\lambda_1+\eta+\mu)dt}$ therefore,

$$
S(t_1) = S(0) \left[\exp^{-\int_0^{t_1} (\lambda_1+\eta+\mu)dt} \right] + \exp^{-\int_0^{t_1} (\lambda_1+\eta+\mu)dt} \times \phi R + \sigma(1-\theta)Q \int_0^t i \left[\exp^{\int_0^x (\lambda_1+\eta+\mu)} \right] dx \geq 0 \tag{16}
$$

Hence, $S(t) \geq 0$ for all time $t > 0$.
From (2b) of the model we have,

$$
\frac{dV}{dt} = \eta S - (\lambda_2 + \mu)V \tag{17}
$$

Rewriting (17), we have

$$
\frac{dV}{dt} + (\lambda_2 + \mu)V = \eta S. \tag{18}
$$

Solving (18) using integration factor method we obtain the equation

$$
\frac{d}{dt}\left[V(t)(\exp^{\int_0^t (\lambda_2+\mu)dt}) \right] = \eta S \left[\exp^{\int_0^t (\lambda_2+\mu)dt} \right] \tag{19}
$$

and integrating (19) from 0 to t_1 we have;

$$\left[V(t_1)(\exp^{\int_0^{t_1}(\lambda_2+\mu)dt}\right] - V(0) = \eta S \int_0^{t_1}\left[\exp^{\int_0^{x}(\lambda_2+\mu)dx}\right] \tag{20}$$

multiply through by $\exp^{-\int_0^{t_1}(\lambda_2+\mu)dt}$

$$V(t_1) = v(0)\left[(\exp^{-\int_0^{t_1}(\lambda_2+\mu)dt}\right] + \left[(\exp^{-\int_0^{t_1}(\lambda_2+\mu)dt}\right] \times \eta S \int_0^{t_1}\left[\exp^{\int_0^{x}(\lambda_2+\mu)}\right]dx \geq 0 \tag{21}$$

Hence, V(t) ≥ 0 for all time $t > 0$.

From (2c) of the model we have the following.

$$\begin{aligned} E(t_1) &= E(0)\left[\left(exp^{-\int_0^{t_1}(\alpha_1+\alpha_2+\alpha_3+\mu\right)dt}\right] + \left[(exp^{-\int_0^{t_1}(\alpha_1+\alpha_2+\alpha_3+\mu)dt}\right]\lambda_1 S \\ &+ \lambda_2 V \int_0^{t_1}\left[E(t)^{\int_0^{t_1}(\alpha_1+\alpha_2+\alpha_3+\mu)}\right]dx \geq 0 \end{aligned} \tag{22}$$

Hence, $E(t) \geq 0$, for all time $t > 0$.

From (2d) of the model we have,

$$\frac{dQ}{dt} = \alpha_1 E - \sigma(1-\theta)Q - (\sigma\theta+\mu)Q \tag{23}$$

we have,

$$\begin{aligned} Q(t_1) &= Q(0)\left[exp^{-\int_0^{t_1}(\sigma+\mu)dt}\right] + \left[exp^{-\int_0^{t_1}(\sigma+\mu)dt}\right] \\ &\times \alpha_1 E \int_0^{t_1}\left[exp^{\int_0^{x}(\sigma+\mu)}\right]dx \geq 0 \end{aligned} \tag{24}$$

Hence, $Q(t) \geq 0$, for all times $t > 0$

From (2e) of the model we have,

$$\frac{dA(t)}{dt} = \alpha_2 E - (\gamma_1\tau+\mu)A - \gamma_1(1-\tau)A \tag{25}$$

$$\begin{aligned} A(t_1) &= A(0)\left[exp^{-\int_0^{t_1}(\gamma_1+\mu)dt}\right] + \left[exp^{-\int_0^{t_1}(\gamma_1+\mu)dt}\right] \\ &\times \alpha_2 E \int_0^{t_1}\left[exp^{\int_0^{x}(\gamma_1+\mu)}\right]dx \geq 0 \end{aligned} \tag{26}$$

Hence, $A(t) \geq 0$, for all times $t > 0$.

From (2f) of the model we have,

$$\frac{dI}{dt} = \alpha_3 E + \sigma\theta Q + \gamma_1(1-\tau)A - \gamma_2(1-\psi)I - (\gamma_2\psi + \mu + \delta)I \tag{27}$$

$$I(t_1) = I(t_0)\left[(exp^{-\int_0^{t_1}(\gamma_2+\delta+\mu)dt})\right] + \left[(exp^{-\int_0^{t_1}(\gamma_2+\delta+\mu)dt})\right] \times \alpha_3 E + \sigma\theta Q + \gamma_1(1-\tau)A\int_0^{t_1}\left[exp^{\int_0^{x}(\gamma_2+\delta+\mu)}\right]dx \geq 0 \tag{28}$$

Hence, $I(t) \geq 0$, for all times $t > 0$.
From (2g) of the model we have,

$$\frac{dT(t)}{dt} = \gamma_2(1-\psi)I - (\gamma_3 + delta + \mu)T \tag{29}$$

$$T(t_1) = T(0)\left[exp^{-\int_0^{t_1}(\gamma_3+\delta+\mu)dt}\right] + \left[exp^{-\int_0^{t_1}(\gamma_3+\delta+\mu)dt}\right] \times \gamma_2(1-\psi)I\int_0^{t_1}\left[(exp^{\int_0^{x}(\gamma_3+\delta+\mu)})\right]dx \tag{30}$$

Hence, $T(t) \geq 0$, for all times $t > 0$.
From (2h) of the model we have,

$$\frac{dR(t)}{dt} = \gamma_1\tau A + \gamma_2\psi I + \gamma_3 T - (\phi + \mu)R \tag{31}$$

$$R(t_1) = R(0)\left[exp^{-\int_0^{t_1}(\phi+\mu)dt}\right] + \left[exp^{-\int_0^{t_1}(\phi+\mu)}\right] \times \gamma_1\tau A + \gamma_2\psi I + \gamma_3 T\int_0^{t_1}\left[exp^{\int_0^{x}(\phi+\mu)}\right]dx \geq 0. \tag{32}$$

Hence, $R(t) \geq 0$, for all times $t > 0$.

Therefore, the solution (S,V,E,Q,A,I,T,R) of the Covid-19 reinfection model (2) with the initial non-negativity condition $16,21,22,24,26,28,30,32$ in the feasible region D remains nonnegative in D for all $t > 0$

4 CONCLUSION

In conclusion, we have successfully developed a comprehensive COVID-19 reinfection model utilizing a mathematical modeling approach. Throughout this study, we meticulously defined the model parameters and variables, laying a solid foundation by clearly stating our assumptions. We rigorously demonstrated the boundedness of the solution, proving that the dynamics of the population under study remains confined within the designated region D. This aspect is critical, as it ensures the realism of the model in reflecting the constraints of a real-world population. Furthermore, our analysis confirmed the non-negativity of the model's solutions, validated by the initial conditions, which affirms that the population consists solely of positive values. This aspect is particularly important when addressing a human population, where it is essential to acknowledge that the number of individuals cannot be negative. Ultimately, our systematic approach not only improves understanding of COVID-19 reinfection dynamics, but also provides a robust framework for future research and public health strategies aimed at managing this ongoing pandemic.

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